

## Generic names in *Magnaporthales*

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**Abstract:** The order *Magnaporthales* comprises about 200 species and includes the economically and scientifically important rice blast fungus and the take-all pathogen of cereals, as well as saprotrophs and endophytes. Recent advances in phylogenetic analyses of these fungi resulted in taxonomic revisions. In this paper we list the 28 currently accepted genera in *Magnaporthales* with their type species and available gene and genome resources. The polyphyletic *Magnaporthe* 1972 is proposed for suppression, and *Pyricularia* 1880 and *Nakataea* 1939 are recommended for protection as the generic names for the rice blast fungus and the rice stem rot fungus, respectively. The rationale for the recommended names is also provided. These recommendations are made by the *Pyricularia/Magnaporthe* Working Group established under the auspices of the International Commission on the Taxonomy of Fungi (ICTF).

### Key words:

*Ascomycota*

*Magnaporthe*

*Nakataea*

one fungus-one name  
pleomorphic fungi

*Pyricularia*

rice blast

take-all

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## INTRODUCTION

*Magnaporthales* (*Sordariomycetes*, *Ascomycota*) contains important pathogens of cereals and grasses, including the rice blast fungus *Pyricularia oryzae* (*Magnaporthe oryzae*), the take-all pathogen of cereals *Gaeumannomyces graminis*, the rice stem rot pathogen *Nakataea oryzae* (*Magnaporthe salvinii*) and the summer patch pathogen of turf grass *Magnaporthiopsis poae* (Cannon 1994, Thongkantha *et al.* 2009). To date, about 200 species have been described in *Magnaporthales*, of which approximately 50 % are pathogens of domesticated and wild monocotyledons.

The rice blast fungus has conidial (asexual) and ascospore (sexual) morphs and the rice stem rot fungus produces sclerotial (asexual), conidial (asexual) and ascospore

(sexual) morphs. Historically, such pleomorphy added to the difficulty in resolving taxonomic and nomenclatural problems associated with these species.

Recent advancement in gene, transcriptome and genome sequencing of *Magnaporthales* fungi resulted in robust phylogenies, which correspond well with the pathogenicity, ecology and biology of these species. However, the phylogenies conflict with certain traditional generic concepts based on morphology. *Magnaporthe* and *Gaeumannomyces*, for example, were shown to be polyphyletic. Taxonomic revisions have been carried out for some of these taxa in recent publications (Luo & Zhang 2013, Klaubauf *et al.* 2014, Luo *et al.* 2015a). In this paper, we list 28 accepted genera in *Magnaporthales* and provide the rationale for the recommended genera if there is competition.

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A list of accepted generic names in *Magnaporthales*, with the type species, is compiled in Table 1 including references that serve as the basis for recognizing these genera. This follows approval of their usage by the *Pyricularia/Magnaporthe* Working Group, without prejudice. Cases that require action to be approved by the Nomenclature Committee for Fungi (NCF) are indicated by an asterisk in that Table.

## RECOMMENDATIONS

(A) = a name typified by an asexual morph, (S) = a name typified by a sexual morph.

### Use *Nakataea* Hara 1939 (A) rather than *Magnaporthe* R.A. Krause & R.K. Webster 1972 (S)

Cattaneo (1876) first named the rice stem rot pathogen as *Sclerotium oryzae* based on the sclerotial morph. In the same paper he also described *Leptosphaeria salvinii*, which was later recognized as the sexual morph of the same fungus (Tullis 1933). Hara (1939) named the conidial morph of the species *Nakataea sigmoidea*. Krause & Webster (1972) then established the new generic name *Magnaporthe*, typified by the ascospore morph, to accommodate the rice stem rot pathogen as *Magnaporthe salvinii*, as necessitated by the nomenclatural rules then in force. *Sclerotium* and *Leptosphaeria* currently belong in *Basidiomycota* and *Dothideomycetes* respectively (Xu et al. 2010), and are therefore not applicable to this sordariomycetous species. *Nakataea* and *Magnaporthe* are congeneric and their type species, *Nakataea sigmoidea* and *Magnaporthe salvinii*, refer to the same species (Krause & Webster 1972). Subsequent to the ending of the separate naming of morphs of the same fungus species in 2011, under Art. 59.1 of the *International Code of Nomenclature for algae, fungi, and plants* (ICN; McNeill et al. 2012), Luo et al. (2013) made a new combination for the rice stem rot fungus as *Nakataea oryzae*, using the oldest legitimate generic name and species epithet. Those authors did not, however, formally propose the rejection or suppression of the later sexually typified names as currently required by Art. 57.2. We note that it is proposed that this requirement be eliminated from the ICN in 2017 (Hawksworth 2015), but it is currently in force.

### Use *Pyricularia oryzae* Cavara 1892 (A) rather than *Magnaporthe oryzae* (Catt.) B.C. Couch 2002 (S)

In 1880, Saccardo established the generic name *Pyricularia* based on the asexually typified *P. grisea* on crabgrass. The rice isolates were designated as *P. oryzae* in 1892 by Cavara, which now is known as the rice blast fungus. Since then, over 50 species have been listed as *Pyricularia* that cause blast diseases of monocotyledonous plants.

The sexual morph of *Pyricularia* was first observed in 1970 from laboratory crossing experiments and believed to belong to *Magnaporthe* because of the similarity in ascospore morphology (Hebert 1970, Barr 1977, Couch & Kohn 2002). However, recent phylogenetic and phylogenomic analyses demonstrated that the sexually typified genus *Magnaporthe* was polyphyletic. The rice blast fungus is not congeneric

with the type species of *Magnaporthe*, *M. salvinii*, and the placement of the rice blast fungus in *Magnaporthe* was based on an incorrect morphological identification (Zhang et al. 2011, Luo & Zhang 2013, Luo et al. 2014, Murata et al. 2014, Luo et al. 2015a). This is not a nomenclatural issue because the generic names *Magnaporthe* and *Pyricularia* are not congeneric and so do not compete for priority.

*Pyricularia* and *Magnaporthe* are currently both widely used generic names, and the rice blast fungus is an economically and scientifically important species that deserves much caution. The *Pyricularia/Magnaporthe* Working Group has considered the possibility of conserving the name *Magnaporthe* over *Pyricularia*. However, such conservation would require a change in the type species of the genus *Magnaporthe*, and would cause numerous name changes for those species currently placed in *Pyricularia*.

The asexually typified generic name *Pyricularia* is the correct name for the rice blast fungus, which corresponds well with pathogenicity and ecological and evolutionary features. The name *Pyricularia oryzae* should therefore be used for the rice blast fungus. The synonym *Magnaporthe oryzae*, can nevertheless continue to be mentioned in publications as "*Pyricularia oryzae* (syn. *Magnaporthe oryzae*)". This practice will help to bridge a potential gap in the literature and knowledge for this important species.

### Use *Clasterosporium* Schwein. 1832 (A) rather than *Clasterosphaeria* Sivan. 1984 (S)

The generic name *Clasterosphaeria*, typified by *C. cyperi*, was established for the sexual morph of *Clasterosporium cyperi* and includes only two names. The generic name *Clasterosporium* based on *C. caricinum* includes 158 names, many of which have been placed in other genera. Whether or not *Clasterosphaeria cyperi* is congeneric with *Clasterosporium caricinum* is not known, although this seems likely given that both occur on *Cyperaceae*. If this is the case, use of the older, more commonly used generic name *Clasterosporium* is recommended.

### Use *Gaeumannomyces* Arx & D.L. Olivier 1952 (S) rather than *Harpophora* Gams 2000 (A)

The generic name *Gaeumannomyces*, typified by *G. graminis*, has long been used for the cause of take-all of wheat disease (Walker 1972, 1980). *Harpophora* was established for phialophora-like species that were known to be asexual morphs related to *Gaeumannomyces* and *Magnaporthe* but did not produce a sexual morph (Gams 2000). With the change to one name, *Harpophora* based on *H. radicicola* is to be considered a synonym of *Gaeumannomyces*, based on phylogeny (Luo et al. 2015b). Given the greater number of species, priority, and numerous reports, we see no reason not to use the first published name, *Gaeumannomyces*.

## ACKNOWLEDGMENTS

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**Table 1.** Accepted generic names in *Magnaporthales* with type species, number of species in each genus, and gene or genomic resources. Names needing approval are indicated by an asterisk (\*).

Taxa	Type species	Number of species	GenBank accession numbers for gene and genome sequence data**
<b>MAGNAPORTHACEAE</b>			
<b><i>Buergenerula</i></b> Syd. in <i>Annls mycol.</i> 34: 392. 1936.	<b><i>Buergenerula biseptata</i></b> (Rostr.) Syd. 1936. ( <i>Metasphaeria biseptata</i> Rostr. 1904).	4	<i>Buergenerula spartinae</i> : transcriptome (SRX798618) (Luo <i>et al.</i> 2015a).
<b><i>Bussabanomyces</i></b> Klaubauf <i>et al.</i> in <i>Stud. Mycol.</i> 79: 100. 2014.	<b><i>Bussabanomyces longisporus</i></b> (Bussaban) Klaubauf <i>et al.</i> 2014. ( <i>Pyricularia longispora</i> Bussaban 2003).	1	<i>Bussabanomyces longisporus</i> : transcriptome (SRX798619) (Luo <i>et al.</i> 2015a).
<b><i>Ceratosphaerella</i></b> Huhndorf <i>et al.</i> in <i>Mycologia</i> 100: 941. 2008.	<b><i>Ceratosphaerella castillensis</i></b> (C.L. Sm.) Huhndorf <i>et al.</i> 2008.	2	<i>Ceratosphaerella castillensis</i> : ITS (EU527997), LSU (EU528003) (Huhndorf <i>et al.</i> 2008).
<b><i>Ceratosphaeria</i></b> Niessl in <i>Verh. nat. Ver. Brünn</i> 14: 203. 1876.	<b><i>Ceratosphaeria lampadophora</i></b> (Berk. & Broome) Niessl 1876.	34	<i>Ceratosphaeria lampadophora</i> : ITS (AY761088), LSU (AY346270) (Huhndorf <i>et al.</i> 2008).
* <b><i>Clasterosporium</i></b> Schwein. in <i>Trans. Am. phil. Soc., New Series</i> 4: 300. 1832.  = <i>Clasterosphaeria</i> Sivan. in <i>Trans. Brit. mycol. Soc.</i> 83: 710. 1984.	<b><i>Clasterosporium caricinum</i></b> Schwein. 1832.	158	
<b><i>Clavatisporella</i></b> K.D. Hyde in <i>Mycotaxon</i> 55: 276. 1995.	<b><i>Clavatisporella musicola</i></b> K.D. Hyde 1995.	1	
<b><i>Falciphora</i></b> J. Luo & N. Zhang in <i>Mycologia</i> 107: 643. 2015.	<b><i>Falciphora oryzae</i></b> (Z.L. Yuan <i>et al.</i> ) J. Luo & N. Zhang 2015.	1	<i>Falciphora oryzae</i> genome (JNVV01000000) (Xu <i>et al.</i> 2014).
<b><i>Gaeumannomyces</i></b> Arx & D.L. Olivier in <i>Trans. Brit. mycol. Soc.</i> 35: 32. 1952.  = <i>Harpophora</i> W. Gams in <i>Stud. Mycol.</i> 45: 192. 2000.	<b><i>Gaeumannomyces graminis</i> var. <i>graminis</i></b> (Sacc.) Arx & D.L. Olivier 1952.	7	<i>Gaeumannomyces graminis</i> var. <i>avenae</i> : transcriptome (SRX798620) (Luo <i>et al.</i> 2015a); <i>Gaeumannomyces graminis</i> var. <i>graminis</i> : transcriptome (SRX798621) (Luo <i>et al.</i> 2015a); <i>Gaeumannomyces graminis</i> var. <i>tritici</i> : genome (ADBI00000000) (Okagaki <i>et al.</i> 2015).
<b><i>Herbampulla</i></b> Scheuer & Nogrsek in <i>Mycotaxon</i> 47: 419. 1993.	<b><i>Herbampulla crassirostris</i></b> Scheuer & Nogrsek 1993	1	
<b><i>Kohlmeyeriopsis</i></b> Klaubauf <i>et al.</i> in <i>Stud. Mycol.</i> 79: 101. 2014.	<b><i>Kohlmeyeriopsis medullaris</i></b> (Kohlm., Volk.-Kohlm. & O.E. Erikss.) Klaubauf <i>et al.</i> 2014.	1	<i>Kohlmeyeriopsis medullaris</i> : SSU(FJ176801), ITS(KM484852), LSU(FJ176801), <i>RPB1</i> (KM485069) (Klaubauf <i>et al.</i> 2014).
<b><i>Magnaporthiopsis</i></b> J. Luo & N. Zhang in <i>Mycologia</i> 105: 1021. 2013.	<b><i>Magnaporthiopsis poae</i></b> (Landsch. & N. Jacks.) J. Luo & N. Zhang 2013.	5	<i>Magnaporthiopsis incrustans</i> : genome (SRX795321), transcriptome (SRX798625) (Luo <i>et al.</i> 2015a); <i>Magnaporthiopsis panicorum</i> : transcriptome (SRX798626) (Luo <i>et al.</i> 2015a); <i>Magnaporthiopsis poae</i> : genome (ADBL01000000) (Okagaki <i>et al.</i> 2015); <i>Magnaporthiopsis rhizophila</i> : genome (SRX798599), transcriptome (SRX798627) (Luo <i>et al.</i> 2015a).
<b><i>Muraeriata</i></b> Huhndorf <i>et al.</i> in <i>Mycologia</i> 100: 948. 2008.	<b><i>Muraeriata collapsa</i></b> Huhndorf, Greif, Mugambi & A.N. Mill. 2008.	2	<i>Muraeriata collapsa</i> : LSU (EU527996) (Huhndorf <i>et al.</i> 2008).

Table 1. (Continued).

Taxa	Type species	Number of species	GenBank accession numbers for gene and genome sequence data**
* <i>Nakataea</i> Hara, Diseases Rice Plant, 2 <sup>nd</sup> : 185. 1939.  = <i>Magnaporthe</i> R.A. Krause & R.K. Webster in Mycologia 64: 110. 1972.	<i>Nakataea oryzae</i> (Catt.) J. Luo & N. Zhang 2013.	7	<i>Nakataea oryzae</i> : genome (SRX798605), transcriptome (SRX798628) (Luo et al. 2015a).
<i>Omnidemptus</i> P.F. Cannon & Alcorn in Mycotaxon 51: 483. 1994.	<i>Omnidemptus affinis</i> P.F. Cannon & Alcorn 1994.	1	<i>Omnidemptus affinis</i> : transcriptome (SRX798629) (Luo et al. 2015a).
<i>Pseudophialophora</i> J. Luo & N. Zhang in Mycologia 106: 581. 2014.	<i>Pseudophialophora eragrostis</i> J. Luo & N. Zhang 2014.	8	<i>Pseudophialophora eragrostis</i> : transcriptome (SRX798634) (Luo et al. 2015a); <i>Pseudophialophora panicorum</i> : transcriptome (SRX798635) (Luo et al. 2015a); <i>Pseudophialophora schizachyrii</i> : transcriptome (SRX798637) (Luo et al. 2015a).
<i>Pyriculariopsis</i> M.B. Ellis, Demat. Hyphom.: 206. 1971.	<i>Pyriculariopsis parasitica</i> (Sacc. & Berl.) M.B. Ellis 1971.	1	<i>Pyriculariopsis parasitica</i> : LSU(DQ341514) (Klaubauf et al. 2014).
<i>Slopeiomyces</i> Klaubauf et al. in Stud. Mycol. 79: 102. 2014.	<i>Slopeiomyces cylindrosporus</i> (D. Hornby et al.) Klaubauf et al. 2014.	1	<i>Slopeiomyces cylindrosporus</i> : transcriptome (SRX798639) (Luo et al. 2015a).
<b>OPHIOCERACEAE</b>			
<i>Ophioceras</i> Sacc., Syll. Fung. 2: 358. 1883.	<i>Ophioceras dolichostomum</i> (Berk. & M.A. Curtis) Sacc. 1883.	33	<i>Ophioceras dolichostomum</i> : genome (SRX798611) (Luo et al. 2015a); <i>Ophioceras commune</i> : transcriptome (SRX798630) (Luo et al. 2015a); <i>Ophioceras leptosporum</i> : transcriptome (SRX798632) (Luo et al. 2015a).
<i>Pseudohalonectria</i> Minoura & T. Muroi in Trans. Mycol. Soc. Japan 19: 132. 1978.	<i>Pseudohalonectria lignicola</i> Minoura & T. Muroi 1978.	13	<i>Pseudohalonectria lignicola</i> : genome (SRX798616), transcriptome (SRX798633) (Luo et al. 2015a).
<b>PYRICULARIACEAE</b>			
<i>Bambusicularia</i> Klaubauf et al. in Stud. Mycol. 79: 104. 2014.	<i>Bambusicularia brunnea</i> Klaubauf et al. 2014.	1	<i>Bambusicularia brunnea</i> : ITS(KM484830), LSU(KM484948), ACT(AB274449), CAL(AB274482), RPB1(KM485043) (Klaubauf et al. 2014).
<i>Barretomyces</i> Klaubauf et al. in Stud. Mycol. 79: 104. 2014.	<i>Barretomyces calathea</i> (D.J. Soares et al.) Klaubauf et al. 2014.	1	<i>Barretomyces calathea</i> : ITS(KM484831), LSU(KM484950), ACT(KM485162), CAL(KM485231), RPB1(KM485045) (Klaubauf et al. 2014).
<i>Deightoniella</i> S. Hughes in Mycol. Pap. 48: 27. 1952.	<i>Deightoniella africana</i> S. Hughes 1952.	20	
<i>Macgarvieomyces</i> Klaubauf et al. in Stud. Mycol. 79: 106. 2014.	<i>Macgarvieomyces borealis</i> (de Hoog & Oorschot) Klaubauf et al. 2014.	2	<i>Macgarvieomyces borealis</i> : SSU(DQ341511), ITS(KM484854), LSU(DQ341511), ACT(KM485170), CAL(KM485239), MCM7(KM009174), RPB1(KM485070), TEF1(KM009198) (Klaubauf et al. 2014, Luo et al. 2015a); <i>Macgarvieomyces juncicola</i> : transcriptome sequenced (SRX798624) (Luo et al. 2015a).
<i>Neopyricularia</i> Klaubauf et al. in Stud. Mycol. 79: 108. 2014.	<i>Neopyricularia commelinicola</i> (M.J. Park & H.D. Shin) Klaubauf et al. 2014.	1	<i>Neopyricularia commelinicola</i> : SSU(KM009211), ITS(FJ850122), LSU(KM484985), ACT(KM485175), CAL(KM485243), MCM7(KM009175), RPB1(KM485087), TEF1(KM009199) (Klaubauf et al. 2014, Luo et al. 2015a).
<i>Proxipyricularia</i> Klaubauf et al. in Stud. Mycol. 79: 109. 2014.	<i>Proxipyricularia zingiberis</i> (Y. Nisik.) Klaubauf et al. 2014.	1	<i>Proxipyricularia zingiberis</i> : ITS(KM484869), LSU(KM484986), ACT(AB274448), CAL(KM485244), RPB1(KM485088) (Klaubauf et al. 2014).



Table 1. (Continued).

Taxa	Type species	Number of species	GenBank accession numbers for gene and genome sequence data**
<i>Pseudopyricularia</i> Klaubauf <i>et al.</i> in Stud. Mycol. 79: 109. 2014.	<i>Pseudopyricularia kyllingae</i> Klaubauf <i>et al.</i> 2014.	3	<i>Pseudopyricularia kyllingae</i> : ITS(KM484876), LSU(KM484992), ACT(AB274451), CAL(AB274484), RPB1(KM485096) (Klaubauf <i>et al.</i> 2014).
<i>Pyricularia</i> Sacc. in Michelia 2: 20. 1880.	<i>Pyricularia grisea</i> Sacc. 1880.	55	<i>Pyricularia grisea</i> : transcriptome (SRX798638) (Luo <i>et al.</i> 2015a); genome (PRJEB7653 at <a href="http://genome.jouy.inra.fr/gemo/">http://genome.jouy.inra.fr/gemo/</a> ) <i>Pyricularia oryzae</i> : Genome (Dean <i>et al.</i> 2005).
<i>Xenopyricularia</i> Klaubauf <i>et al.</i> in Stud. Mycol. 79: 116. 2014.	<i>Xenopyricularia zizaniicola</i> (Hashioka) Klaubauf <i>et al.</i> 2014.	1	<i>Xenopyricularia zizaniicola</i> : transcriptome (SRX798640) (Luo <i>et al.</i> 2015a).

\*\* Unpublished genome data are not listed.

## REFERENCES

- Barr ME (1977) *Magnaporthe*, *Telimenella*, and *Hyponectria* (*Physosporrellaceae*). *Mycologia* **69**: 952–966.
- Cannon PF (1994) The newly recognized family *Magnaporthaceae* and its interrelationships. *Systema Ascomycetum* **13**:25–42.
- Cattaneo A (1876) Sulla *Sclerotium oryzae*, nuovo parassità vegetale, che ha devastato nel corrente anno molto risaje di Lombardia e del Novarese. *Rendic. R. Lombard., Milano, 2 ser.* **9**: 801–807.
- Couch BC, Kohn LM (2002) A multilocus gene genealogy concordant with host preference indicates segregation of a new species, *Magnaporthe oryzae*, from *M. grisea*. *Mycologia* **94**: 683–693.
- Dean RA, Talbot NJ, Ebbole DJ, Farman ML, Mitchell TK, *et al.* (2005) The genome sequence of the rice blast fungus *Magnaporthe grisea*. *Nature* **434**: 980–986.
- Gams W (2000) *Phialophora* and some similar morphologically little-differentiated anamorphs of divergent ascomycetes. *Studies in Mycology* **45**: 187–199.
- Hara, K (1939) *The Diseases of the Rice-plant*. 2nd edn. Gifu: Japanese Society for Fungi.
- Hebert TT (1970) The perfect stage of *Pyricularia grisea*. *Phytopathology* **61**: 83–87.
- Huhndorf SM, Greif M, Mugambi GK, Miller AN (2008) Two new genera in the *Magnaporthaceae*, a new addition to *Ceratosphaeria* and two new species of *Lentomitella*. *Mycologia* **100**: 940–955.
- Klaubauf S, Tharreau D, Fournier E, Groenewald JZ, Crous PW, *et al.* (2014) Resolving the polyphyletic nature of *Pyricularia* (*Pyriculariaceae*). *Studies in Mycology* **79**: 85–120.
- Krause RA, Webster RK (1972) The morphology, taxonomy, and sexuality of the rice stem rot fungus, *Magnaporthe salvinii* (*Leptosphaeria salvinii*). *Mycologia* **64**: 103–114.
- Luo J, Qiu H, Cai G, Wagner NE, Bhattacharya D, *et al.* (2015a) Phylogenomic analysis uncovers the evolutionary history of nutrition and infection mode in rice blast fungus and other *Magnaporthales*. *Scientific Reports* **5**: 9448.
- Luo J, Walsh E, Zhang N (2014) Four new species in *Magnaporthaceae* from grass roots in New Jersey Pine Barrens. *Mycologia* **106**: 580–588.
- Luo J, Walsh E, Zhang N (2015b) Toward monophyletic generic concepts in *Magnaporthales*: species with *Harpophora* asexual states. *Mycologia* **107**: 641–646.
- Luo J, Zhang N (2013) *Magnaporthiopsis*, a new genus in *Magnaporthaceae* (Ascomycota). *Mycologia* **105**: 1019–1029.
- McNeill J, Barrie FF, Buck WR, Demoulin V, Greuter W, *et al.* (2012) *International code of nomenclature for algae, fungi, and plants (Melbourne Code)*. [Regnum Vegetabile no. 154.] Königstein: Koeltz Scientific Books.
- Murata N, Aoki T, Kusaba M, Tosa Y, Chuma I (2014) Various species of *Pyricularia* constitute a robust clade distinct from *Magnaporthe salvinii* and its relatives in *Magnaporthaceae*. *Journal of General Plant Pathology* **80**: 66–72.
- Okagaki LH, Nunes CC, Sailsbery J, Clay B, Brown D, *et al.* (2015) Genome sequences of three phytopathogenic species of the *Magnaporthaceae* family of fungi. *G3 (Bethesda)* **5**: 2539–2545.
- Thongkantha S, Jeewon R, Vijaykrishna D, Lumyong S, *et al.* (2009) Molecular phylogeny of *Magnaporthaceae* (*Sordariomycetes*) with a new species *Ophioceras Chiangdaoense* from *Dracaena loureiroi* in Thailand. *Fungal Diversity* **34**:157–173.
- Tullis EC (1933) *Leptosphaeria salvinii*, the ascigerous stage of *Helminthosporium sigmoideum* and *Sclerotium oryzae*. *Journal of Agricultural Research* **47**: 675–687.
- Walker J (1972) Type studies on *Gaeumannomyces graminis* and related fungi. *Transactions of the British Mycological Society* **58**: 427–457.
- Walker J (1980) *Gaeumannomyces*, *Linocarpon*, *Ophiobolus* and several genera of scolecospored ascomycetes and *Phialophora* conidial states, with a note on hyphopodia. *Mycotaxon*. **11**:1–129
- Xu XH, Su ZZ, Wang C, Kubicek CP, Feng XX, *et al.* (2014) The rice endophyte *Harpophora oryzae* genome reveals evolution from a pathogen to a mutualistic endophyte. *Scientific Reports* **4**: 5783.
- Xu Z, Harrington TC, Gleason ML, Batzer JC (2010) Phylogenetic placement of plant pathogenic *Sclerotium* species among teleomorph genera. *Mycologia* **102**: 337–346.
- Zhang N, Zhao S, Shen QR (2011) A six-gene phylogeny reveals the evolution of mode of infection in the rice blast fungus and allied species. *Mycologia* **103**: 1267–1276.